



#4

SEQUENCE LISTING

<110> Hauptmann, Rudolph
Himmler, Adolph
Maurer-Fogy, Ingrid
Stratowa, Christian

<120> TNF Receptors, TNF Binding Proteins and DNAs Coding for
Them

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<141> 2001-07-03

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<151> 1993-11-17

<150> 07/821,750
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<170> PatentIn Ver. 2.0

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<222> (88)..(120)
<223> Portion of TNF-BP pro protein cleaved by
extracellular proteases following secretion.

<220>
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<222> (606)..(633)
<223> Portion of TNF-BP pro protein cleaved by

extracellular proteases following secretion.

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gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct	96
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro	
20 25 30	
cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa	144
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys	
35 40 45	
tat atc cac cct caa aat aat tgc att tgc tgt acc aag tgc cac aaa	192
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys	
50 55 60	
gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac	240
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp	
65 70 75 80	
tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc	288
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu	
85 90 95	
aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg	336
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val	
100 105 110	
gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg	384
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg	
115 120 125	
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130 135 140	
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145 150 155 160	
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aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg	576
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr	
180 185 190	
aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca	624
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser	
195 200 205	
ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt	672
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu	

210	215	220	
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225	230	235	240
tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag			768
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu			
	245	250	255
ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc			816
Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser			
	260	265	270
ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg			864
Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val			
	275	280	285
ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt			912
Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys			
	290	295	300
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Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly			
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Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn			
	325	330	335
ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac			1056
Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp			
	340	345	350
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Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln			
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tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc			1248
Tyr Ser Met Leu Ala Thr Trp Arg Arg Thr Pro Arg Arg Glu Ala			
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Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly			
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Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro			
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1368

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 50 55 60
 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
 65 70 75 80
 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
 85 90 95
 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
 100 105 110
 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
 115 120 125
 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
 130 135 140
 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
 145 150 155 160
 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
 165 170 175
 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
 180 185 190
 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
 195 200 205
 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
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 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
 225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
 245 250 255
 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
 260 265 270
 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
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 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
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 370 375 380
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 405 410 415
 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
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Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys	
20 25 30	
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Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser	
35 40 45	
ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa	192
Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys	
50 55 60	
tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac	240
Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp	
65 70 75 80	
cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg	288
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp	
85 90 95	
agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg	336
Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly	
100 105 110	
acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc	384
Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys	
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cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac	432
His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn	
130 135 140	
tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag	480
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 35 40 45
 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
 50 55 60

Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
 65 70 75 80
 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
 85 90 95
 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
 100 105 110
 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
 115 120 125
 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
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 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly
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ctggacagac cgagtcccgg gaagccccag cactgccgct gccacactgc cctgagccca 180
aatgggcgag tgagaggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 233
                               Met Gly Leu Ser Thr Val Pro
                               1                               5

gac ctg ctg ctg cca ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281
Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr
          10                      15                      20

ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329
Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys
          25                      30                      35

aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377
Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
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tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425
Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
          60                      65                      70

tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
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tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
          90                      95                      100

aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
          105                      110                      115

gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat 617
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
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Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn
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ggg acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc 713
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr
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Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe			
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Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser			
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Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr			
	315	320	325
gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac			1241
Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp			
	330	335	340
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Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu			
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<223> Description of Artificial Sequence: cDNA insert of
lambdaTNF-BP15 and pTNF-BP15 vectors

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His	Leu	Gly	Asp	Arg	Glu	Lys	Arg	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	35	40	45	
Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	50	55	60	
Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	65	70	75	80
Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	85	90	95	
Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	100	105	110	
Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	115	120	125	
Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	130	135	140	
Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	145	150	155	160
Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	165	170	175	
Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	180	185	190	
Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	195	200	205	
Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu	210	215	220	
Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys	225	230	235	240
Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys	Glu	245	250	255	
Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn	Pro	Ser	260	265	270	
Phe	Ser	Pro	Thr	Pro	Gly	Phe	Thr	Pro	Thr	Leu	Gly	Phe	Ser	Pro	Val	275	280	285	

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
 290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
 305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
 325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
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Leu Arg Trp
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 caacgacccc cgccattga cgtcaataat gacgtatggt cccatagtaa cgccaatagg 180
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<210> 14

<211> 2173

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (245)..(1630)

<220>

<223> Description of Artificial Sequence: raTNF-R8

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 gggctcacgc tgccaacacc cgggccacct ggtccgatcg tcttacttca ttcaccageg 180
 ttgccaattg ctgcctgtc cccagcccca atgggggagtg gagagaggcc actgccggcc 240

ggac atg ggt ctc ccc atc gtg cct ggc ctg ctg ctg tca ctg gtg ctc	289
Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu	
1 5 10 15	
ctg gct ctg ctg atg ggg ata cac cca tca ggg gtc acc gga ctg gtt	337
Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val	
20 25 30	
cct tct ctt ggt gac cgg gag aag agg gat aat ttg tgt ccc cag gga	385
Pro Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly	
35 40 45	
aag tat gcc cat cca aag aat aat tcc atc tgc tgc acc aag tgc cac	433
Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His	
50 55 60	
aaa gga acc tac ttg gtg agt gac tgt cca agc cca ggg cag gaa aca	481
Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr	
65 70 75	
gtc tgc gag ctc tct cat aaa ggc acc ttt aca gct tcg cag aac cac	529
Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His	
80 85 90 95	
gtc aga cag tgt ctc agt tgc aag aca tgt cgg aaa gaa atg ttc cag	577
Val Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln	
100 105 110	
gtg gag att tct cct tgc aaa gct gac atg gac acc gtg tgt ggc tgc	625
Val Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys	
115 120 125	
aag aag aac caa ttc cag cgc tac ctg agt gag acg cat ttc cag tgt	673
Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys	
130 135 140	
gtg gac tgc agc ccc tgc ttc aat ggc acc gtg aca atc ccc tgt aag	721
Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys	
145 150 155	
gag aaa cag aac acc gtg tgt aac tgc cac gca gga ttc ttt cta agc	769
Glu Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser	
160 165 170 175	
gga aat gag tgc acc cct tgc agc cac tgc aag aaa aat cag gaa tgt	817
Gly Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys	
180 185 190	
atg aag ctg tgc cta cct cca gtt gca aat gtc aca aac ccc cag gac	865
Met Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp	
195 200 205	
tca ggt act gcc gtg ctg ttg cct ctg gtt atc ttc cta ggt ctt tgc	913
Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys	
210 215 220	
ctt tta ttc ttt atc tgc atc agt cta ctg tgc cga tat ccc cag tgg	961

Leu	Leu	Phe	Phe	Ile	Cys	Ile	Ser	Leu	Leu	Cys	Arg	Tyr	Pro	Gln	Trp		
225						230					235						
agg	ccc	agg	gtc	tac	tcc	atc	att	tgt	agg	gat	tca	gct	cct	gtc	aaa	1009	
Arg	Pro	Arg	Val	Tyr	Ser	Ile	Ile	Cys	Arg	Asp	Ser	Ala	Pro	Val	Lys		
240					245					250					255		
gag	gtg	gag	ggg	gaa	gga	att	gtt	act	aag	ccc	cta	act	cca	gcc	tct	1057	
Glu	Val	Glu	Gly	Glu	Gly	Ile	Val	Thr	Lys	Pro	Leu	Thr	Pro	Ala	Ser		
				260					265					270			
atc	cca	gcc	ttc	agc	ccc	aac	ccc	ggc	ttc	aac	ccc	act	ctg	ggc	ttc	1105	
Ile	Pro	Ala	Phe	Ser	Pro	Asn	Pro	Gly	Phe	Asn	Pro	Thr	Leu	Gly	Phe		
			275					280					285				
agc	acc	acc	cca	cgc	ttc	agt	cat	cct	gtc	tcc	agt	acc	ccc	atc	agc	1153	
Ser	Thr	Thr	Pro	Arg	Phe	Ser	His	Pro	Val	Ser	Ser	Thr	Pro	Ile	Ser		
		290					295					300					
ccc	gtc	ttc	ggg	cct	agt	aac	tgg	cac	aac	ttc	gtg	cca	cct	gta	aga	1201	
Pro	Val	Phe	Gly	Pro	Ser	Asn	Trp	His	Asn	Phe	Val	Pro	Pro	Val	Arg		
	305					310					315						
gag	gtg	gtc	cca	acc	cag	ggg	gct	gac	cct	ctc	ctc	tac	gga	tcc	ctc	1249	
Glu	Val	Val	Pro	Thr	Gln	Gly	Ala	Asp	Pro	Leu	Leu	Tyr	Gly	Ser	Leu		
320					325				330					335			
aac	cct	gtg	cca	atc	ccc	gcc	cct	gtt	cgg	aaa	tgg	gaa	gac	gtc	gtc	1297	
Asn	Pro	Val	Pro	Ile	Pro	Ala	Pro	Val	Arg	Lys	Trp	Glu	Asp	Val	Val		
				340					345					350			
gcg	gcc	cag	cca	caa	cgg	ctt	gac	act	gca	gac	cct	gcg	atg	ctg	tat	1345	
Ala	Ala	Gln	Pro	Gln	Arg	Leu	Asp	Thr	Ala	Asp	Pro	Ala	Met	Leu	Tyr		
			355				360						365				
gct	gtg	gtg	gat	ggc	gtg	cct	ccg	aca	cgc	tgg	aag	gag	ttc	atg	cgg	1393	
Ala	Val	Val	Asp	Gly	Val	Pro	Pro	Thr	Arg	Trp	Lys	Glu	Phe	Met	Arg		
		370					375					380					
ctc	ctg	ggg	ctg	agc	gag	cac	gag	atc	gag	cgg	ttg	gag	ctg	cag	aac	1441	
Leu	Leu	Gly	Leu	Ser	Glu	His	Glu	Ile	Glu	Arg	Leu	Glu	Leu	Gln	Asn		
	385					390					395						
ggg	cgt	tgc	ctc	cgc	gag	gct	cat	tac	agc	atg	ctg	gaa	gcc	tgg	cgg	1489	
Gly	Arg	Cys	Leu	Arg	Glu	Ala	His	Tyr	Ser	Met	Leu	Glu	Ala	Trp	Arg		
400					405					410				415			
cgc	cgc	aca	ccg	cga	cac	gag	gcc	acg	ctg	gac	gta	gtg	ggc	cgc	gtg	1537	
Arg	Arg	Thr	Pro	Arg	His	Glu	Ala	Thr	Leu	Asp	Val	Val	Gly	Arg	Val		
				420					425					430			
ctt	tgc	gac	atg	aac	ctg	cgt	ggc	tgc	ctg	gag	aac	atc	cgc	gag	act	1585	
Leu	Cys	Asp	Met	Asn	Leu	Arg	Gly	Cys	Leu	Glu	Asn	Ile	Arg	Glu	Thr		
			435				440						445				
cta	gaa	agc	cct	gcc	cac	tcg	tcc	acg	acc	cac	ctc	ccg	cga	taa		1630	
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				

450

455

460

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 ttc 2173

<210> 15

<211> 461

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: raTNF-R8

<400> 15

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Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro
 20 25 30

Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly Lys
 35 40 45

Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 50 55 60

Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val
 65 70 75 80

Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val
 85 90 95

Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val
 100 105 110

Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys Lys
 115 120 125

Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys Val

130					135					140					
Asp	Cys	Ser	Pro	Cys	Phe	Asn	Gly	Thr	Val	Thr	Ile	Pro	Cys	Lys	Glu
145					150					155					160
Lys	Gln	Asn	Thr	Val	Cys	Asn	Cys	His	Ala	Gly	Phe	Phe	Leu	Ser	Gly
				165					170					175	
Asn	Glu	Cys	Thr	Pro	Cys	Ser	His	Cys	Lys	Lys	Asn	Gln	Glu	Cys	Met
			180					185					190		
Lys	Leu	Cys	Leu	Pro	Pro	Val	Ala	Asn	Val	Thr	Asn	Pro	Gln	Asp	Ser
		195					200					205			
Gly	Thr	Ala	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Leu	Gly	Leu	Cys	Leu
	210						215					220			
Leu	Phe	Phe	Ile	Cys	Ile	Ser	Leu	Leu	Cys	Arg	Tyr	Pro	Gln	Trp	Arg
225							230					235			240
Pro	Arg	Val	Tyr	Ser	Ile	Ile	Cys	Arg	Asp	Ser	Ala	Pro	Val	Lys	Glu
				245					250					255	
Val	Glu	Gly	Glu	Gly	Ile	Val	Thr	Lys	Pro	Leu	Thr	Pro	Ala	Ser	Ile
			260					265					270		
Pro	Ala	Phe	Ser	Pro	Asn	Pro	Gly	Phe	Asn	Pro	Thr	Leu	Gly	Phe	Ser
		275					280					285			
Thr	Thr	Pro	Arg	Phe	Ser	His	Pro	Val	Ser	Ser	Thr	Pro	Ile	Ser	Pro
		290					295					300			
Val	Phe	Gly	Pro	Ser	Asn	Trp	His	Asn	Phe	Val	Pro	Pro	Val	Arg	Glu
305							310					315			320
Val	Val	Pro	Thr	Gln	Gly	Ala	Asp	Pro	Leu	Leu	Tyr	Gly	Ser	Leu	Asn
				325					330					335	
Pro	Val	Pro	Ile	Pro	Ala	Pro	Val	Arg	Lys	Trp	Glu	Asp	Val	Val	Ala
			340					345					350		
Ala	Gln	Pro	Gln	Arg	Leu	Asp	Thr	Ala	Asp	Pro	Ala	Met	Leu	Tyr	Ala
		355					360					365			
Val	Val	Asp	Gly	Val	Pro	Pro	Thr	Arg	Trp	Lys	Glu	Phe	Met	Arg	Leu
		370					375					380			
Leu	Gly	Leu	Ser	Glu	His	Glu	Ile	Glu	Arg	Leu	Glu	Leu	Gln	Asn	Gly
385							390					395			400
Arg	Cys	Leu	Arg	Glu	Ala	His	Tyr	Ser	Met	Leu	Glu	Ala	Trp	Arg	Arg
				405					410					415	
Arg	Thr	Pro	Arg	His	Glu	Ala	Thr	Leu	Asp	Val	Val	Gly	Arg	Val	Leu
			420					425					430		
Cys	Asp	Met	Asn	Leu	Arg	Gly	Cys	Leu	Glu	Asn	Ile	Arg	Glu	Thr	Leu

435

440

445

Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg
 450 455 460

<210> 16

<211> 2141

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (213)..(1580)

<220>

<223> Description of Artificial Sequence: human TNF-R in
 1TNF-R2

<400> 16

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ctggacagac cgagtcccgg gaagccccag cactgccgct gccacactgc cctgagccca 180

katgggggag tgagaggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 233
 Met Gly Leu Ser Thr Val Pro
 1 5

gac ctg ctg ctg cca ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281
 Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr
 10 15 20

ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329
 Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys
 25 30 35

aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377
 Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
 40 45 50 55

tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425
 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
 60 65 70

tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473
 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
 75 80 85

tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521
 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
 90 95 100

aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569
 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
 105 110 115

gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat	617
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr	
120 125 130 135	
tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat	665
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn	
140 145 150	
ggg acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc	713
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr	
155 160 165	
tgc cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt	761
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser	
170 175 180	
aac tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att	809
Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile	
185 190 195	
gag aat gtt aag ggc act gag gac tca ggc acc aca gtg ctg ttg ccc	857
Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro	
200 205 210 215	
ctg gtc att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt	905
Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly	
220 225 230	
tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt	953
Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val	
235 240 245	
tgt ggg aaa tcg aca cct gaa aaa gag ggg gag ctt gaa gga act act	1001
Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr	
250 255 260	
act aag ccc ctg gcc cca aac cca agc ttc agt ccc act cca ggc ttc	1049
Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe	
265 270 275	
acc ccc acc ctg ggc ttc agt ccc gtg ccc agt tcc acc ttc acc tcc	1097
Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser	
280 285 290 295	
agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc	1145
Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg	
300 305 310	
aga gag gtg gca cca ccc tat cag ggg gct gac ccc atc ctt gcg aca	1193
Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr	
315 320 325	
gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac	1241
Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp	
330 335 340	

agc gcc cac aag cca cag agc cta gac act gat gac ccc gcg acg ctg 1289
 Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu
 345 350 355

 tac gcc gtg gtg gag aac gtg ccc ccg ttg cgc tgg aag gaa ttc gtg 1337
 Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val
 360 365 370 375

 cgg cgc cta ggg ctg agc gac cac gag atc gat cgg ctg gag ctg cag 1385
 Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln
 380 385 390

 aac ggg cgc tgc ctg cgc gag gcg caa tac agc atg ctg gcg acc tgg 1433
 Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp
 395 400 405

 agg cgg cgc acg ccg cgg cgc gag gcc acg ctg gag ctg ctg gga cgc 1481
 Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg
 410 415 420

 gtg ctc cgc gac atg gac ctg ctg ggc tgc ctg gag gac atc gag gag 1529
 Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu
 425 430 435

 gcg ctt tgc ggc ccc gcc gcc ctc ccg ccc gcg ccc agt ctt ctc aga 1577
 Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg
 440 445 450 455

 tga ggctgcgccc ctgcgggcag ctctaaggac cgtcctgcga gatcgccctc 1630

 caaccccact tttttctgga aaggaggggt cctgcagggg caagcaggag ctagcagccg 1690
 cctacttggt gctaaccct cgatgtacat agcttttctc agctgcctgc gcgcgcgcca 1750
 cagtcagcgc tgtgcgcgcg gagagaggtg cgcctggtgc tcaagagcct gagtgggtgg 1810
 tttgcgagga tgagggacgc tatgcctcat gcccgttttg ggtgtcctca ccagcaaggc 1870
 tgctcggggg cccctgggtc gtccctgagc ctttttcaca gtgcataagc agtttttttt 1930
 gtttttgttt tgttttgttt tgtttttaaa tcaatcatgt tacactaata gaaacttggc 1990
 actcctgtgc cctctgctg gacaagcaca tagcaagctg aactgtccta aggcaggggc 2050
 gagcacggaa caatggggcc ttcagctgga gctgtggact tttgtacata cactaaaatt 2110
 ctgaagttaa aaaaaaaaaa aaaaggaatt c 2141

<210> 17

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human TNF-R in

1TNF-R2

<400> 17

Met	Gly	Leu	Ser	Thr	Val	Pro	Asp	Leu	Leu	Leu	Pro	Leu	Val	Leu	Leu	1	5	10	15
Glu	Leu	Leu	Val	Gly	Ile	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Leu	Val	Pro	20	25	30	
His	Leu	Gly	Asp	Arg	Glu	Lys	Arg	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	35	40	45	
Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	50	55	60	
Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	65	70	75	80
Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	85	90	95	
Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	100	105	110	
Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	115	120	125	
Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	130	135	140	
Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	145	150	155	160
Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	165	170	175	
Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	180	185	190	
Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	195	200	205	
Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu	210	215	220	
Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys	225	230	235	240
Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys	Glu	245	250	255	
Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn	Pro	Ser	260	265	270	
Phe	Ser	Pro	Thr	Pro	Gly	Phe	Thr	Pro	Thr	Leu	Gly	Phe	Ser	Pro	Val	275	280	285	

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
 290 295 300
 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
 305 310 315 320
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
 325 330 335
 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
 340 345 350
 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
 355 360 365
 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
 370 375 380
 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
 385 390 395 400
 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
 405 410 415
 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
 420 425 430
 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
 435 440 445
 Pro Ala Pro Ser Leu Leu Arg
 450 455

<210> 18
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: N-terminal
 amino acid sequence of protein purified from urine
 (main sequence)

<220>
 <221> UNSURE
 <222> (4)
 <223> Identity of "Xaa" could not be determined.

<400> 18
 Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln
 1 5 10

<210> 19
 <211> 9
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: N-terminal
amino acid sequence of protein purified from urine
(sudsidiary sequence)

<220>

<221> UNSURE

<222> (7)

<223> Identity of "Xaa" could not be determined.

<400> 19

Leu Val Pro His Leu Gly Xaa Arg Glu
1 5

<210> 20

<211> 151

<212> DNA

<213> Homo sapiens

<400> 20

caggggaaaa tattcaccct caaataattc gatttgctgt accaagtgcc acaaaggaaa 60
ctacttgtag aatgactgtc caggcccggg gcaggatacg gactgcaggg agtgtgagag 120
cggctccttc acagcctcag aaaacaacaa g 151

<210> 21

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 21

Asp Ser Val Cys Pro Gln Gly Lys
1 5

<210> 22

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>

<221> UNSURE

<222> (1)..(2)

<223> Identity of "Xaa" could not be determined.

<400> 22
Xaa Xaa Leu Ser Cys Ser Lys
1 5

<210> 23
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 23
Asp Thr Val Cys Gly Cys Arg
1 5

<210> 24
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 24
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
1 5 10

<210> 25
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 25
Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys
1 5 10

<210> 26
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>
 <221> UNSURE
 <222> (6)
 <223> Identity of "Xaa" could not be determined.

<220>
 <221> UNSURE
 <222> (10)..(12)
 <223> Identity of "Xaa" could not be determined.

<400> 26
 Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys
 1 5 10

<210> 27
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

<400> 27
 Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys
 1 5 10

<210> 28
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

<400> 28
 Leu Val Pro His Leu Gly Asp Arg
 1 5

<210> 29
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

<400> 29
 Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg
 1 5 10 15

<210> 30
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 30
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln
1 5 10

<210> 31
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>
<221> UNSURE
<222> (9)..(11)
<223> Identity of "Xaa" could not be determined.

<400> 31
Glu Met Gly Gln Val Glu Ile Ser Xaa Xaa Xaa Val Asp
1 5 10

<210> 32
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 32
Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp
1 5 10 15

Thr Val Cys Gly
20

<210> 33
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic

cleavage peptide

<220>

<221> UNSURE

<222> (6)

<223> Identity of "Xaa" could not be determined.

<220>

<221> UNSURE

<222> (18)

<223> Identity of "Xaa" could not be determined.

<400> 33

Tyr	Ile	His	Pro	Gln	Xaa	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys
1				5					10					15	

Gly Xaa Tyr

<210> 34

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<220>

<221> UNSURE

<222> (16)..(17)

<223> Identity of "Xaa" could not be determined.

<400> 34

Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Xaa
1				5					10					15	

Xaa Arg

<210> 35

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 35

Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn
1				5			

<210> 36

<211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

 <220>
 <221> UNSURE
 <222> (7)
 <223> Identity of "Xaa" could not be determined.

 <400> 36
 Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Leu Arg
 1 5 10

 <210> 37
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

 <400> 37
 Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn
 1 5 10

 <210> 38
 <211> 13
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

 <400> 38
 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln
 1 5 10

 <210> 39
 <211> 7
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> Description of Artificial Sequence: TNF-BP tryptic
 cleavage peptide

 <400> 39
 Gln Gly Lys Tyr Ile His Pro

<210> 40
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 40
caaggtaa atattcatcc 20

<210> 41
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 41
cagggtaagt acatccatcc 20

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 42
caaggtaa atatacatcc 20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 43
caaggcaa atattcatcc 20

<210> 44
<211> 20

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 44
 cagggcaagt acatccaccc 20

 <210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 45
 caaggcaa atatacatcc 20

 <210> 46
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 46
 caaggaaa atattcatcc 20

 <210> 47
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 47
 cagggaaagt acatccaccc 20

 <210> 48
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization

probe

<400> 48
caaggaaaat atatacatcc 20

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 49
caagggaaaat atattcatcc 20

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 50
caggggaagt acatccaccc 20

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 51
caagggaaaat atatacatcc 20

<210> 52
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 52
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys
1 5 10

<210> 53
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 53
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys
1 5 10

<210> 54
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 54
Phe Thr Ala Ser Glu Asn Asn Lys
1 5

<210> 55
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-BP tryptic
cleavage peptide

<400> 55
Phe Thr Ala Ser Cys Asn Asn Lys
1 5

<210> 56
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hybridization
probe

<400> 56
aaatgacgga gactcttggt gttcctaggg

30

<210> 57
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 57
 aagtggcgta gtcttttggt gttcctaggg 30

 <210> 58
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 58
 aaatgtcgga gactcttggt gttcctaggg 30

 <210> 59
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 59
 aaatgacggt cactcttggt gttcctaggg 30

 <210> 60
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Hybridization
 probe

 <400> 60
 aagtggcggt ctcttttggt gttcctaggg 30

 <210> 61
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hybridization
 probe

<400> 61
 aaatgtcggg cactcttggt gttcctaggg 30

<210> 62
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hybridization
 probe

<400> 62
 aaatgacgga gaacattggt gttcctaggg 30

<210> 63
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hybridization
 probe

<400> 63
 aagtggcgta gtactttggt gttcctaggg 30

<210> 64
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hybridization
 probe

<400> 64
 aaatgtcgga gaacattggt gttcctaggg 30

<210> 65
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hybridization
 probe

<400> 65

aaatgacggt caacattggt gttcctaggg

30

<210> 66

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization
probe

<400> 66

aagtggcggt ctactttggt gttcctaggg

30

<210> 67

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization
probe

<400> 67

aaatgtcggt caacattggt gttcctaggg

30

<210> 68

<211> 158

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(153)

<400> 68

cag ggg aaa tat att cac cct caa aat aat tcg att tgc tgt acc aag 48

Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys

1

5

10

15

tgc cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag 96

Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln

20

25

30

gat acg gac tgc agg gag tgt gag agc ggc tcc ttc aca gcc tca gaa 144

Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu

35

40

45

aac aac aag gatcc

158

Asn Asn Lys

50

<210> 69

<211> 51
<212> PRT
<213> Homo sapiens

<400> 69
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys
1 5 10 15
Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln
20 25 30
Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu
35 40 45
Asn Asn Lys
50

<210> 70
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-1786

<400> 70
ggaattcagc ctgaatggcg aatggg 26

<210> 71
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-1729

<400> 71
cctcgagcgt tgctggcggt tttcc 25

<210> 72
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-1733

<400> 72
ggtcgacatt gattattgac tag 23

<210> 73
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-1734

<400> 73
ggaattcctt aggaatacag cgg 23

<210> 74
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutagenesis
primer EBI-1751

<400> 74
gtacttgaac tcgttcctg 19

<210> 75
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutagenesis
primer EBI-1857

<400> 75
ggcaagggca gcagccgg 18

<210> 76
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide EBI-1823

<400> 76
agcttctgca ggtcgacatc gatggatcgg tacctcgagc ggccgcgaat tct 53

<210> 77
<211> 54
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide EBI-1829

<400> 77

ctagagaatt cgcggccgct cgaggtaccg gatccatoga tgcgacctg caga 54

<210> 78

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide EBI-1820

<400> 78

agctctagag attcgcggcc gctcgaggta ccgcatccat cgatgtcgac ctgcagaagc 60

ttg

63

<210> 79

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide EBI-1821

<400> 79

ctagcaagct tctgcaggtc gacatcgatg gatccggtag ctcgagcggc cgcgaattct 60

ctag

64

<210> 80

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
EBI-1986

<400> 80

caggatccga gtctcaaccc tcaac 25

<210> 81

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer
EBI-1929

<400> 81
gggaattcct tatcaattct caatctgggg taggcacaac ttc 43

<210> 82
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-2452

<400> 82
cacagtcgac ttacatttgc ttctgacaca actgtgttca ctagcaacct caaacagaca 60
ccatgggcct ctccaccgtg c 81

<210> 83
<211> 17
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR primer
EBI-1922

<400> 83
gaggctgcaa ttgaagc 17

<210> 84
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-2316

<400> 84
attcgtgcgg cgcctag 17

<210> 85
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-2467

<400> 85
gtcggtagca ccaagga

17

<210> 86
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
EBI-1986

<400> 86
gttttcccag tcacgac

17

<210> 87
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Sequencing
primer EBI-2112

<400> 87
gtccaattat gtcacacc

18